

SEQUENZPROTOKOLL

<110> Poustka, et al.

<120> Protein (TP) That is Involved in the Development of the Nervous System

<130> 4121-129

<140> US/09/914,549

<141> 2001-08-24

<150> PCT/DE00/00583

<151> 2000-02-28

<150> DE 199 08 423.8

<151> 1999-02-26

<160> 39

<170> PatentIn Ver. 2.0

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<212> DNA

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acc cag caa gat atg cag tcc agt ctg gca gcc aga tat gca act cag      95
Thr Gln Gln Asp Met Gln Ser Ser Leu Ala Ala Arg Tyr Ala Thr Gln
          20              25              30

tct aat cac agt gga att gca acc agt caa aaa aag cct act agg ctt      143
Ser Asn His Ser Gly Ile Ala Thr Ser Gln Lys Lys Pro Thr Arg Leu
          35              40              45

cca ggg ccc tct agg gtg cct gct gca gga agc agc agc aag gtc cag      191
Pro Gly Pro Ser Arg Val Pro Ala Ala Gly Ser Ser Ser Lys Val Gln
          50              55              60

gga gcc tct aat tta aat agg aga agt cag agc ttt aac agc att gac      239
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Lys

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242

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Asn His Ser Gly Ile Ala Thr Ser Gln Lys Lys Pro Thr Arg Leu Pro
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Gly Pro Ser Arg Val Pro Ala Ala Gly Ser Ser Ser Lys Val Gln Gly
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Ser Thr Leu Ser Glu Arg Tyr Thr Pro Ser Ser Arg Gln Ala Asn Gln
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gaa gag ggc aaa gag tgg ttg cgt tct cat tct act gga ggg ctt cag 144
Glu Glu Gly Lys Glu Trp Leu Arg Ser His Ser Thr Gly Gly Leu Gln
35 40 45

gac act ggc aac cag 159
Asp Thr Gly Asn Gln
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 Leu Leu Lys Ala Glu Asn Asp Arg Leu Lys Val Ala Pro Gly Pro Ser

tca ggc tcc act cca ggg cag gtc cct gga tca tct gca tta tct tcc 142
 Ser Gly Ser Thr Pro Gly Gln Val Pro Gly Ser Ser Ala Leu Ser Ser

cca cgc cgc tcc cta ggc ctg gca ctc acc cat tcc ttc ggc ccc agt 190
 Pro Arg Arg Ser Leu Gly Leu Ala Leu Thr His Ser Phe Gly Pro Ser

ctt gca gac aca gac ctg tca ccc atg gat ggc atc agt act tgt ggt 238
 Leu Ala Asp Thr Asp Leu Ser Pro Met Asp Gly Ile Ser Thr Cys Gly

cca aag gag gaa gtg acc ctc cgg gtg gtg gtg agg atg ccc ccg cag 286
 Pro Lys Glu Glu Val Thr Leu Arg Val Val Val Arg Met Pro Pro Gln

cac atc atc aaa ggg gac ttg aag cag cag gaa ttc ttc ctg ggc tgt His Ile Ile Lys Gly Asp Leu Lys Gln Gln Glu Phe Phe Leu Gly Cys	334
agc aag gtc agt gga aaa gtt gac tgg aag atg ctg gat gaa gct gtt Ser Lys Val Ser Gly Lys Val Asp Trp Lys Met Leu Asp Glu Ala Val	382
ttc caa gtg ttc aag gac tat att tct aaa atg gac cca gcc tct acc Phe Gln Val Phe Lys Asp Tyr Ile Ser Lys Met Asp Pro Ala Ser Thr	430
ctg gga cta agc act gag tcc atc cat ggc tac agc atc agc cac gtg Leu Gly Leu Ser Thr Glu Ser Ile His Gly Tyr Ser Ile Ser His Val	478
aaa cga gtg ttg gat gca gag ccc ccc gag atg cct cct tgc cgt cga Lys Arg Val Leu Asp Ala Glu Pro Pro Glu Met Pro Pro Cys Arg Arg	526
ggt gtc aat aac ata tca gtc tcc ctc aaa ggt ctg aag gag aaa tgc Gly Val Asn Asn Ile Ser Val Ser Leu Lys Gly Leu Lys Glu Lys Cys	574
gtc gac agc ctg gtg ttc gag acg ctg atc ccc aag ccg atg atg cag Val Asp Ser Leu Val Phe Glu Thr Leu Ile Pro Lys Pro Met Met Gln	622
cac tac ata agc ctc ctg ctg aag cac cgg cgc ctc gtc ctc tgc ggc His Tyr Ile Ser Leu Leu Leu Lys His Arg Arg Leu Val Leu Ser Gly	670
ccc agc ggc acg ggc aag acc tac ctg acc aat cgc ttg gcc gag tac Pro Ser Gly Thr Gly Lys Thr Tyr Leu Thr Asn Arg Leu Ala Glu Tyr	718
ctg gtg gag cgc tct ggc cgt gag gtc aca gag ggc atc gtc agc acc Leu Val Glu Arg Ser Gly Arg Glu Val Thr Glu Gly Ile Val Ser Thr	766
ttc aac atg cac cag cag tct tgc aag gat ctg caa ctg tat ctt tcc Phe Asn Met His Gln Gln Ser Cys Lys Asp Leu Gln Leu Tyr Leu Ser	814
aac cta gcc aac cag ata gac cgg gaa aca gga att ggg gat gtg ccc Asn Leu Ala Asn Gln Ile Asp Arg Glu Thr Gly Ile Gly Asp Val Pro	862
ctg gtg att cta ttg gat gac ctg agt gaa gca ggc tcc atc agt gag Leu Val Ile Leu Leu Asp Asp Leu Ser Glu Ala Gly Ser Ile Ser Glu	910
ttg gtc aat ggg gcc ctc acc tgc aag tat cat aaa tgt ccc tat att Leu Val Asn Gly Ala Leu Thr Cys Lys Tyr His Lys Cys Pro Tyr Ile	958

ata ggt acc acc aat cag cct gta aaa atg aca ccc aac cat ggc ttg Ile Gly Thr Thr Asn Gln Pro Val Lys Met Thr Pro Asn His Gly Leu	1006
cac ttg agc ttc agg atg ttg acc ttc tcc aac aac gtg gag cca gcc His Leu Ser Phe Arg Met Leu Thr Phe Ser Asn Asn Val Glu Pro Ala	1054
aat ggc ttc ctg gtt cgt tac ctg agg agg aag ctg gta gag tca gac Asn Gly Phe Leu Val Arg Tyr Leu Arg Arg Lys Leu Val Glu Ser Asp	1102
agc gac atc aat gcc aac aag gaa gag ctg ctt cgg gtg ctc gac tgg Ser Asp Ile Asn Ala Asn Lys Glu Glu Leu Leu Arg Val Leu Asp Trp	1150
gta ccc aag ctg tgg tat cat ctc cac acc ttc ctt gag aag cac agc Val Pro Lys Leu Trp Tyr His Leu His Thr Phe Leu Glu Lys His Ser	1198
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atc att ccc tat cta cag gaa gga gcc aag gat ggg ata aag gtc cat Ile Ile Pro Tyr Leu Gln Glu Gly Ala Lys Asp Gly Ile Lys Val His	1342
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ctt ccc tgg cca tca gcc caa caa gac caa tca aag ctg tac cac ctg Leu Pro Trp Pro Ser Ala Gln Gln Asp Gln Ser Lys Leu Tyr His Leu	1438
ccc cca ccc acc gtg ggc cct cac agc att gcc tca cct ccc gag gat Pro Pro Pro Thr Val Gly Pro His Ser Ile Ala Ser Pro Pro Glu Asp	1486
agg aca gtc aaa gac agc acc cca agt tct ctg gac tca gat cct ctg Arg Thr Val Lys Asp Ser Thr Pro Ser Ser Leu Asp Ser Asp Pro Leu	1534
atg gcc atg ctg ctg aaa ctt caa gaa gct gcc aac tac att gag tct Met Ala Met Leu Leu Lys Leu Gln Glu Ala Ala Asn Tyr Ile Glu Ser	1582
cca gat cga gaa acc atc ctg gac ccc aac ctt cag gca aca ctt Pro Asp Arg Glu Thr Ile Leu Asp Pro Asn Leu Gln Ala Thr Leu	1627

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<210> 6
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		20						25					30		
Gly	Ser	Thr	Pro	Gly	Gln	Val	Pro	Gly	Ser	Ser	Ala	Leu	Ser	Ser	Pro
		35					40					45			
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		50				55					60				
Ala	Asp	Thr	Asp	Leu	Ser	Pro	Met	Asp	Gly	Ile	Ser	Thr	Cys	Gly	Pro
65					70					75				80	
Lys	Glu	Glu	Val	Thr	Leu	Arg	Val	Val	Val	Arg	Met	Pro	Pro	Gln	His
			85					90						95	
Ile	Ile	Lys	Gly	Asp	Leu	Lys	Gln	Gln	Glu	Phe	Phe	Leu	Gly	Cys	Ser

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Lys Val Ser Gly Lys Val Asp Trp Lys Met Leu Asp Glu Ala Val Phe 115	120	125
Gln Val Phe Lys Asp Tyr Ile Ser Lys Met Asp Pro Ala Ser Thr Leu 130	135	140
Gly Leu Ser Thr Glu Ser Ile His Gly Tyr Ser Ile Ser His Val Lys 145	150	155
Arg Val Leu Asp Ala Glu Pro Pro Glu Met Pro Pro Cys Arg Arg Gly 165	170	175
Val Asn Asn Ile Ser Val Ser Leu Lys Gly Leu Lys Glu Lys Cys Val 180	185	190
Asp Ser Leu Val Phe Glu Thr Leu Ile Pro Lys Pro Met Met Gln His 195	200	205
Tyr Ile Ser Leu Leu Leu Lys His Arg Arg Leu Val Leu Ser Gly Pro 210	215	220
Ser Gly Thr Gly Lys Thr Tyr Leu Thr Asn Arg Leu Ala Glu Tyr Leu 225	230	235
Val Glu Arg Ser Gly Arg Glu Val Thr Glu Gly Ile Val Ser Thr Phe 245	250	255
Asn Met His Gln Gln Ser Cys Lys Asp Leu Gln Leu Tyr Leu Ser Asn 260	265	270
Leu Ala Asn Gln Ile Asp Arg Glu Thr Gly Ile Gly Asp Val Pro Leu 275	280	285
Val Ile Leu Leu Asp Asp Leu Ser Glu Ala Gly Ser Ile Ser Glu Leu 290	295	300
Val Asn Gly Ala Leu Thr Cys Lys Tyr His Lys Cys Pro Tyr Ile Ile 305	310	315
Gly Thr Thr Asn Gln Pro Val Lys Met Thr Pro Asn His Gly Leu His 325	330	335
Leu Ser Phe Arg Met Leu Thr Phe Ser Asn Asn Val Glu Pro Ala Asn 340	345	350
Gly Phe Leu Val Arg Tyr Leu Arg Arg Lys Leu Val Glu Ser Asp Ser 355	360	365
Asp Ile Asn Ala Asn Lys Glu Glu Leu Leu Arg Val Leu Asp Trp Val 370	375	380
Pro Lys Leu Trp Tyr His Leu His Thr Phe Leu Glu Lys His Ser Thr 385	390	395
Ser Asp Phe Leu Ile Gly Pro Cys Phe Phe Leu Ser Cys Pro Ile Gly		400

405

410

415

Ile Glu Asp Phe Arg Thr Trp Phe Ile Asp Leu Trp Asn Asn Ser Ile
 420 425 430

Ile Pro Tyr Leu Gln Glu Gly Ala Lys Asp Gly Ile Lys Val His Gly
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Gln Lys Ala Ala Trp Glu Asp Pro Val Glu Trp Val Arg Asp Thr Leu
 450 455 460

Pro Trp Pro Ser Ala Gln Gln Asp Gln Ser Lys Leu Tyr His Leu Pro
 465 470 475 480

Pro Pro Thr Val Gly Pro His Ser Ile Ala Ser Pro Pro Glu Asp Arg
 485 490 495

Thr Val Lys Asp Ser Thr Pro Ser Ser Leu Asp Ser Asp Pro Leu Met
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Ala Met Leu Leu Lys Leu Gln Glu Ala Ala Asn Tyr Ile Glu Ser Pro
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Asp Arg Glu Thr Ile Leu Asp Pro Asn Leu Gln Ala Thr Leu
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<211> 2568

<212> DNA

<213> mouse

<220>

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<223> (1)..(1695)

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 Leu Asn Ser Ala His Gln Leu Asp Gln Leu Arg Glu Thr Met His Asn

atg cag ttg gag gtg gac ctg ctg aaa gca gag aat gac cgg ctg aag 144
 Met Gln Leu Glu Val Asp Leu Leu Lys Ala Glu Asn Asp Arg Leu Lys

gtt gcc ccc ggc ccc tcc tca ggc tgc act cca ggg cag gtc cct ggg 192
 Val Ala Pro Gly Pro Ser Ser Gly Cys Thr Pro Gly Gln Val Pro Gly

tca tcg gct ctg tgc tcc cct cga cgt tcc ctg ggc ctt gca ctc agc Ser Ser Ala Leu Ser Ser Pro Arg Arg Ser Leu Gly Leu Ala Leu Ser	240
cat cct ttc agt cct agt ctc aca gac aca gac ctc tca ccc atg gat His Pro Phe Ser Pro Ser Leu Thr Asp Thr Asp Leu Ser Pro Met Asp	288
ggc atc agc acc tgt ggt tca aag gaa gag gtg acc ctg cgg gtg gtg Gly Ile Ser Thr Cys Gly Ser Lys Glu Glu Val Thr Leu Arg Val Val	336
gtc cgg atg ccg ccc cag cac atc atc aaa ggg gac tta aag cag cag Val Arg Met Pro Pro Gln His Ile Ile Lys Gly Asp Leu Lys Gln Gln	384
gag ttc ttc ctg ggt tgc agc aag gtc agt ggc aaa gtt gac tgg aag Glu Phe Phe Leu Gly Cys Ser Lys Val Ser Gly Lys Val Asp Trp Lys	432
atg ctg gat gaa gcc gtt ttc caa gtg ttc aag gac tac att tct aaa Met Leu Asp Glu Ala Val Phe Gln Val Phe Lys Asp Tyr Ile Ser Lys	480
atg gac cca gcc tca acc ctg gga ctg agc act gag tcc ata cat ggc Met Asp Pro Ala Ser Thr Leu Gly Leu Ser Thr Glu Ser Ile His Gly	528
tat agc ctc agc cac gtg aaa cga gtg ctg gat gct gag ccc cca gag Tyr Ser Leu Ser His Val Lys Arg Val Leu Asp Ala Glu Pro Pro Glu	576
atg cct cct tgc cgc cga ggt gtc aat aac ata tca gtc gct ctc aaa Met Pro Pro Cys Arg Arg Gly Val Asn Asn Ile Ser Val Ala Leu Lys	624
ggt ctg aaa gag aag tgt gtc gac agc ctg gtg ttc gag acg ctt atc Gly Leu Lys Glu Lys Cys Val Asp Ser Leu Val Phe Glu Thr Leu Ile	672
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cgc ctg gtg ctc tcc ggc ccc agt ggc acc ggc aag acc tac ttg acc Arg Leu Val Leu Ser Gly Pro Ser Gly Thr Gly Lys Thr Tyr Leu Thr	768
aat cgg cta gcc gag tac ctg gtg gag cgc tcc ggc cgc gag gtc acg Asn Arg Leu Ala Glu Tyr Leu Val Glu Arg Ser Gly Arg Glu Val Thr	816
gat ggc atc gtc agc act ttc aac atg cac cag cag tct tgc aag gat Asp Gly Ile Val Ser Thr Phe Asn Met His Gln Gln Ser Cys Lys Asp	864

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ggg ata ggg gat gtg ccc ttg gtg atc ctc ctg gat gat ctg agt gaa Gly Ile Gly Asp Val Pro Leu Val Ile Leu Leu Asp Asp Leu Ser Glu	960
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ttc ctg gag aag cac agc acc tcg gac ttc ctc att ggc cct tgc ttc Phe Leu Glu Lys His Ser Thr Ser Asp Phe Leu Ile Gly Pro Cys Phe	1296
ttc ctg tcc tgt ccc att ggc atc gag gac ttc cgg acc tgg ttc att Phe Leu Ser Cys Pro Ile Gly Ile Glu Asp Phe Arg Thr Trp Phe Ile	1344
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tca aag ctc tac cac ctg ccc ccg cct tct gtg ggc ccc cac agc act Ser Lys Leu Tyr His Leu Pro Pro Pro Ser Val Gly Pro His Ser Thr	1536

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ctc gac tca gat ccc ctg atg gcc atg cta ctg aaa ctc caa gaa gct Leu Asp Ser Asp Pro Leu Met Ala Met Leu Leu Lys Leu Gln Glu Ala	1632
gcc aac tac att gag tca cca gat cga gag act atc ctg gac ccc aac Ala Asn Tyr Ile Glu Ser Pro Asp Arg Glu Thr Ile Leu Asp Pro Asn	1680
ctc cag gcg aca ctc tgagggcccg gcagtcactg tcaccctgga gggcagaagg Leu Gln Ala Thr Leu	1735
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<210> 8
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<400> 8

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	20						25						30		

Met Gln Leu Glu Val Asp Leu Leu Lys Ala Glu Asn Asp Arg Leu Lys
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 50 55 60
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 65 70 75 80
 His Pro Phe Ser Pro Ser Leu Thr Asp Thr Asp Leu Ser Pro Met Asp
 85 90 95
 Gly Ile Ser Thr Cys Gly Ser Lys Glu Glu Val Thr Leu Arg Val Val
 100 105 110
 Val Arg Met Pro Pro Gln His Ile Ile Lys Gly Asp Leu Lys Gln Gln
 115 120 125
 Glu Phe Phe Leu Gly Cys Ser Lys Val Ser Gly Lys Val Asp Trp Lys
 130 135 140
 Met Leu Asp Glu Ala Val Phe Gln Val Phe Lys Asp Tyr Ile Ser Lys
 145 150 155 160
 Met Asp Pro Ala Ser Thr Leu Gly Leu Ser Thr Glu Ser Ile His Gly
 165 170 175
 Tyr Ser Leu Ser His Val Lys Arg Val Leu Asp Ala Glu Pro Pro Glu
 180 185 190
 Met Pro Pro Cys Arg Arg Gly Val Asn Asn Ile Ser Val Ala Leu Lys
 195 200 205
 Gly Leu Lys Glu Lys Cys Val Asp Ser Leu Val Phe Glu Thr Leu Ile
 210 215 220
 Pro Lys Pro Met Met Gln His Tyr Ile Ser Leu Leu Leu Lys His Arg
 225 230 235 240
 Arg Leu Val Leu Ser Gly Pro Ser Gly Thr Gly Lys Thr Tyr Leu Thr
 245 250 255
 Asn Arg Leu Ala Glu Tyr Leu Val Glu Arg Ser Gly Arg Glu Val Thr
 260 265 270
 Asp Gly Ile Val Ser Thr Phe Asn Met His Gln Gln Ser Cys Lys Asp
 275 280 285
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 Gly Ile Gly Asp Val Pro Leu Val Ile Leu Leu Asp Asp Leu Ser Glu
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 Ala Gly Ser Ile Ser Glu Leu Val Asn Gly Ala Leu Thr Cys Lys Tyr

325

330

335

His Lys Cys Pro Tyr Ile Ile Gly Thr Thr Asn Gln Pro Val Lys Met
340 345 350

Thr Pro Asn His Gly Leu His Leu Ser Phe Arg Met Leu Thr Phe Ser
355 360 365

Asn Asn Val Glu Pro Ala Asn Gly Phe Leu Val Arg Tyr Leu Arg Arg
370 375 380

Lys Leu Val Glu Ser Asp Ser Asp Val Asn Ala Asn Lys Glu Glu Leu
385 390 395 400

Leu Arg Val Leu Asp Trp Val Pro Lys Leu Trp Tyr His Leu His Thr
405 410 415

Phe Leu Glu Lys His Ser Thr Ser Asp Phe Leu Ile Gly Pro Cys Phe
420 425 430

Phe Leu Ser Cys Pro Ile Gly Ile Glu Asp Phe Arg Thr Trp Phe Ile
435 440 445

Asp Leu Trp Asn Asn Ser Ile Ile Pro Tyr Leu Gln Glu Gly Ala Lys
450 455 460

Asp Gly Ile Lys Val His Gly Gln Lys Ala Ala Trp Glu Asp Pro Val
465 470 475 480

Glu Trp Val Arg Asp Thr Leu Pro Trp Pro Ser Ala Gln Gln Asp Gln
485 490 495

Ser Lys Leu Tyr His Leu Pro Pro Pro Ser Val Gly Pro His Ser Thr
500 505 510

Ala Ser Pro Pro Glu Asp Arg Thr Val Lys Asp Ser Thr Pro Asn Ser
515 520 525

Leu Asp Ser Asp Pro Leu Met Ala Met Leu Leu Lys Leu Gln Glu Ala
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<212> DNA

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46

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Glu Val Asn Gly Arg Ala Ile Pro Asn Leu Thr Ser Arg Pro Ser Pro

94

atg acc tgg aga ctg ggt caa gcg tgc cct cgt cta cag gct gga gat
Met Thr Trp Arg Leu Gly Gln Ala Cys Pro Arg Leu Gln Ala Gly Asp

142

gcc ccc tcc atg ggc gct gga tat tct cga agc ggt acc agc cga ttc
Ala Pro Ser Met Gly Ala Gly Tyr Ser Arg Ser Gly Thr Ser Arg Phe

190

atc cac acg gat ccc tcc agg ttt atg tat acc acg cct ctc cgc cga
Ile His Thr Asp Pro Ser Arg Phe Met Tyr Thr Thr Pro Leu Arg Arg

238

gct gct gtc tcg cgt ctg gga aac atg tca caa ata gat atg agc gag
Ala Ala Val Ser Arg Leu Gly Asn Met Ser Gln Ile Asp Met Ser Glu

286

aaa gca agc agt gac ctg gat gtg tct tct gaa gtg gat gtt ggt gga
Lys Ala Ser Ser Asp Leu Asp Val Ser Ser Glu Val Asp Val Gly Gly

334

tac atg agc gat ggt gat atc ctt ggg aag agt ctg aga gcg gat gat
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382

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430

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478

aga ggc gtt cac gat gtg aca gtg gac gca gac agc tgg gat gac agc
Arg Gly Val His Asp Val Thr Val Asp Ala Asp Ser Trp Asp Asp Ser

526

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574

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622

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tcg aca aca gat gag acc tgg gat agt cct gag gag ctg aag aaa gcc Ser Thr Thr Asp Glu Thr Trp Asp Ser Pro Glu Glu Leu Lys Lys Ala	718
gag gga gat tgt gac agc cat ggt gac gga gcc gcc aag tgg aag ggt Glu Gly Asp Cys Asp Ser His Gly Asp Gly Ala Ala Lys Trp Lys Gly	766
gct act tct gga ctt gct gaa gac tcg gag aag aca ggg cag aaa gcc Ala Thr Ser Gly Leu Ala Glu Asp Ser Glu Lys Thr Gly Gln Lys Ala	814
agc ctg tct gtg tct cag aca ggc tcc tgg agg aga ggc atg tct gcc Ser Leu Ser Val Ser Gln Thr Gly Ser Trp Arg Arg Gly Met Ser Ala	862
cag gga gga act cca gct aca gct agg cag aaa acc agc aca agt gca Gln Gly Gly Thr Pro Ala Thr Ala Arg Gln Lys Thr Ser Thr Ser Ala	910
ctc aag acc cct ggg aag aca gat gat gcc aaa gct tcc gag aaa ggg Leu Lys Thr Pro Gly Lys Thr Asp Asp Ala Lys Ala Ser Glu Lys Gly	958
aaa act cct ctc aaa gga tca tcc ttg caa agg tct cct tca gat gca Lys Thr Pro Leu Lys Gly Ser Ser Leu Gln Arg Ser Pro Ser Asp Ala	1006
ggg aaa agc agc ggg gat gaa ggg aaa aag cca ccg tca ggc att gga Gly Lys Ser Ser Gly Asp Glu Gly Lys Lys Pro Pro Ser Gly Ile Gly	1054
aga tcg aca gcc agc agt tct ttt gga tac aag aag cca agt ggt gta Arg Ser Thr Ala Ser Ser Ser Phe Gly Tyr Lys Lys Pro Ser Gly Val	1102
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tca gct aca ctg ggg aaa atc ccc aaa tcc gct gcc att ggt ggg aag Ser Ala Thr Leu Gly Lys Ile Pro Lys Ser Ala Ala Ile Gly Gly Lys	1198
tcc aat gca gga agg aaa acc agc ctg gac ggg tcc cag aat caa gat Ser Asn Ala Gly Arg Lys Thr Ser Leu Asp Gly Ser Gln Asn Gln Asp	1246
gat gtt gtc ctg cac gtg agc tcg aag acc acc ctc cag tac cgt agt Asp Val Val Leu His Val Ser Ser Lys Thr Thr Leu Gln Tyr Arg Ser	1294
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tca gct ggg gcc acc acc tcc aaa ctg aga gaa ccg act aag atc ggc Ser Ala Gly Ala Thr Thr Ser Lys Leu Arg Glu Pro Thr Lys Ile Gly	1438
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act gag ggg gcg aag tcc tcc tca gta gtg ctc agc cct agt acc tct Thr Glu Gly Ala Lys Ser Ser Ser Val Val Leu Ser Pro Ser Thr Ser	1726
tta gcc cga caa ggc agt ctg gag tca ccg tcg tcc ggt acg gga agc Leu Ala Arg Gln Gly Ser Leu Glu Ser Pro Ser Ser Gly Thr Gly Ser	1774
atg ggc agt gct ggt ggg ctg agt ggc agc agc agc cct ctc ttc aat Met Gly Ser Ala Gly Gly Leu Ser Gly Ser Ser Ser Pro Leu Phe Asn	1822
aaa ccc tca gac cta act aca gat gtt ata agc tta agt cac tcc ttg Lys Pro Ser Asp Leu Thr Thr Asp Val Ile Ser Leu Ser His Ser Leu	1870
gct tcc agc cca gcg tcg gtt cac tct ttc aca tcc ggt ggg ctt gtg Ala Ser Ser Pro Ala Ser Val His Ser Phe Thr Ser Gly Gly Leu Val	1918
tgg gct gcc aat ctg agc agt tcc tct gcc ggc agc aag gac act cca Trp Ala Ala Asn Leu Ser Ser Ser Ser Ala Gly Ser Lys Asp Thr Pro	1966
agt tac cag tcc atg act agt ctc cat acg agc tct gag tcc att gac Ser Tyr Gln Ser Met Thr Ser Leu His Thr Ser Ser Glu Ser Ile Asp	2014

ctg ccc ctc agc cat cat ggc tcc ctg tct gga ctg acc aca ggc act Leu Pro Leu Ser His His Gly Ser Leu Ser Gly Leu Thr Thr Gly Thr	2062
cac gag gtg cag agc ctg ctc atg aga acg ggt agt gtg aga tct act His Glu Val Gln Ser Leu Leu Met Arg Thr Gly Ser Val Arg Ser Thr	2110
ctc tca gaa aga tac acc cca tca tct cgg cag gcc aac caa gaa gaa Leu Ser Glu Arg Tyr Thr Pro Ser Ser Arg Gln Ala Asn Gln Glu Glu	2158
ggc aaa gag tgg ctg cga tgc cat tcc act ggc ggg ctg cag gat act Gly Lys Glu Trp Leu Arg Ser His Ser Thr Gly Gly Leu Gln Asp Thr	2206
ggc aac cag tct ccc ttg gtc tcc cct tct gcc atg tca tgc tca gcc Gly Asn Gln Ser Pro Leu Val Ser Pro Ser Ala Met Ser Ser Ser Ala	2254
acc gga aaa tat cac ttt tcc aac ttg gtg agt ccc acc aac ctc tcc Thr Gly Lys Tyr His Phe Ser Asn Leu Val Ser Pro Thr Asn Leu Ser	2302
cag ttt aac ctg cct gca ccc agt atg atg cgc tcc agc agt atc ccc Gln Phe Asn Leu Pro Ala Pro Ser Met Met Arg Ser Ser Ser Ile Pro	2350
gcc cag gac tcc tcc ttc gac ctc tat gat gat gcc cag ctt tgc ggt Ala Gln Asp Ser Ser Phe Asp Leu Tyr Asp Asp Ala Gln Leu Cys Gly	2398
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tca ttc aga gac agc atg gag gaa gtt cat ggc tct tca ctg tca ttg Ser Phe Arg Asp Ser Met Glu Glu Val His Gly Ser Ser Leu Ser Leu	2494
gtc tcc agc aca tca tcc ctt tac tct acg gct gaa gag aag gct cat Val Ser Ser Thr Ser Ser Leu Tyr Ser Thr Ala Glu Glu Lys Ala His	2542
tca gag caa atc cat aag cta cgg aga gaa ctg gtt gcc tcc cag gag Ser Glu Gln Ile His Lys Leu Arg Arg Glu Leu Val Ala Ser Gln Glu	2590
aaa gtc gct acc ctc acg tct cag ctg tca gca aat gct cac ctt gta Lys Val Ala Thr Leu Thr Ser Gln Leu Ser Ala Asn Ala His Leu Val	2638
gca gct ttt gaa aag agt tta ggg aat atg act ggc cgt ttg caa agt Ala Ala Phe Glu Lys Ser Leu Gly Asn Met Thr Gly Arg Leu Gln Ser	2686
cta acc atg aca gcg gaa caa aag gaa tct gag ctt atc gaa ctg cgg	2734

Leu Thr Met Thr Ala Glu Gln Lys Glu Ser Glu Leu Ile Glu Leu Arg

gaa acc att gaa atg ttg aag gcc cag aac tct gct gcc caa gca gcc 2782
Glu Thr Ile Glu Met Leu Lys Ala Gln Asn Ser Ala Ala Gln Ala Ala

att cag gga gca ctg aat ggc cca gac cac cct ccc aaa gat ctc cgc 2830
Ile Gln Gly Ala Leu Asn Gly Pro Asp His Pro Pro Lys Asp Leu Arg

atc aga aga cag cac tcc tct gaa agt gtt tct agt atc aac agc gca 2878
Ile Arg Arg Gln His Ser Ser Glu Ser Val Ser Ser Ile Asn Ser Ala

acg agc cat tcc agc att ggc agt ggt aat gat gct gac tcc aag aaa 2926
Thr Ser His Ser Ser Ile Gly Ser Gly Asn Asp Ala Asp Ser Lys Lys

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<212> PRT
<213> Mouse

<400> 20

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Val Asn Gly Arg Ala Ile Pro Asn Leu Thr Ser Arg Pro Ser Pro Met
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Thr Trp Arg Leu Gly Gln Ala Cys Pro Arg Leu Gln Ala Gly Asp Ala
35 40 45

Pro Ser Met Gly Ala Gly Tyr Ser Arg Ser Gly Thr Ser Arg Phe Ile
50 55 60

His Thr Asp Pro Ser Arg Phe Met Tyr Thr Thr Pro Leu Arg Arg Ala
65 70 75 80

Ala Val Ser Arg Leu Gly Asn Met Ser Gln Ile Asp Met Ser Glu Lys
85 90 95

Ala Ser Ser Asp Leu Asp Val Ser Ser Glu Val Asp Val Gly Gly Tyr
100 105 110

Met Ser Asp Gly Asp Ile Leu Gly Lys Ser Leu Arg Ala Asp Asp Ile
115 120 125

Asn Ser Gly Tyr Met Thr Asp Gly Gly Leu Asn Leu Tyr Thr Arg Ser
130 135 140

Leu Asn Arg Val Pro Asp Thr Ala Thr Ser Arg Asp Val Ile Gln Arg
145 150 155 160

Gly Val His Asp Val Thr Val Asp Ala Asp Ser Trp Asp Asp Ser Ser
 165 170 175
 Ser Val Ser Ser Gly Leu Ser Asp Thr Leu Asp Asn Ile Ser Thr Asp
 180 185 190
 Asp Leu Asn Thr Thr Ser Ser Ile Ser Ser Tyr Ser Asn Ile Thr Val
 195 200 205
 Pro Ser Arg Lys Asn Thr Gln Leu Lys Thr Asp Ala Glu Lys Arg Ser
 210 215 220
 Thr Thr Asp Glu Thr Trp Asp Ser Pro Glu Glu Leu Lys Lys Ala Glu
 225 230 235 240
 Gly Asp Cys Asp Ser His Gly Asp Gly Ala Ala Lys Trp Lys Gly Ala
 245 250 255
 Thr Ser Gly Leu Ala Glu Asp Ser Glu Lys Thr Gly Gln Lys Ala Ser
 260 265 270
 Leu Ser Val Ser Gln Thr Gly Ser Trp Arg Arg Gly Met Ser Ala Gln
 275 280 285
 Gly Gly Thr Pro Ala Thr Ala Arg Gln Lys Thr Ser Thr Ser Ala Leu
 290 295 300
 Lys Thr Pro Gly Lys Thr Asp Asp Ala Lys Ala Ser Glu Lys Gly Lys
 305 310 315 320
 Thr Pro Leu Lys Gly Ser Ser Leu Gln Arg Ser Pro Ser Asp Ala Gly
 325 330 335
 Lys Ser Ser Gly Asp Glu Gly Lys Lys Pro Pro Ser Gly Ile Gly Arg
 340 345 350
 Ser Thr Ala Ser Ser Ser Phe Gly Tyr Lys Lys Pro Ser Gly Val Gly
 355 360 365
 Ala Ser Thr Met Ile Thr Ser Ser Gly Ala Thr Ile Thr Ser Gly Ser
 370 375 380
 Ala Thr Leu Gly Lys Ile Pro Lys Ser Ala Ala Ile Gly Gly Lys Ser
 385 390 395 400
 Asn Ala Gly Arg Lys Thr Ser Leu Asp Gly Ser Gln Asn Gln Asp Asp
 405 410 415
 Val Val Leu His Val Ser Ser Lys Thr Thr Leu Gln Tyr Arg Ser Leu
 420 425 430
 Pro Arg Pro Ser Lys Ser Ser Thr Ser Gly Ile Pro Gly Arg Gly Gly
 435 440 445
 His Arg Ser Ser Thr Ser Ser Ile Asp Ser Asn Val Ser Ser Lys Ser

450
 Ala Gly Ala Thr Thr Ser Lys Leu Arg Glu Pro Thr Lys Ile Gly Ser 480
 465 470 475
 Gly Arg Ser Ser Pro Val Thr Val Asn Gln Thr Asp Lys Glu Lys Glu 495
 485 490
 Lys Val Ala Val Ser Asp Ser Glu Ser Val Ser Leu Ser Gly Ser Pro 510
 500 505
 Lys Ser Ser Pro Thr Ser Ala Ser Ala Cys Gly Thr Gln Gly Leu Arg 525
 515 520
 Gln Pro Gly Ser Lys Tyr Pro Asp Ile Ala Ser Pro Thr Phe Arg Arg 540
 530 535
 Leu Phe Gly Ala Lys Ala Gly Gly Lys Ser Ala Ser Ala Pro Asn Thr 560
 545 550 555
 Glu Gly Ala Lys Ser Ser Ser Val Val Leu Ser Pro Ser Thr Ser Leu 575
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 Ala Arg Gln Gly Ser Leu Glu Ser Pro Ser Ser Gly Thr Gly Ser Met 590
 580 585
 Gly Ser Ala Gly Gly Leu Ser Gly Ser Ser Ser Pro Leu Phe Asn Lys 605
 595 600
 Pro Ser Asp Leu Thr Thr Asp Val Ile Ser Leu Ser His Ser Leu Ala 620
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 Ser Ser Pro Ala Ser Val His Ser Phe Thr Ser Gly Gly Leu Val Trp 640
 625 630 635
 Ala Ala Asn Leu Ser Ser Ser Ser Ala Gly Ser Lys Asp Thr Pro Ser 655
 645 650
 Tyr Gln Ser Met Thr Ser Leu His Thr Ser Ser Glu Ser Ile Asp Leu 670
 660 665
 Pro Leu Ser His His Gly Ser Leu Ser Gly Leu Thr Thr Gly Thr His 685
 675 680
 Glu Val Gln Ser Leu Leu Met Arg Thr Gly Ser Val Arg Ser Thr Leu 700
 690 695
 Ser Glu Arg Tyr Thr Pro Ser Ser Arg Gln Ala Asn Gln Glu Glu Gly 720
 705 710 715
 Lys Glu Trp Leu Arg Ser His Ser Thr Gly Gly Leu Gln Asp Thr Gly 735
 725 730
 Asn Gln Ser Pro Leu Val Ser Pro Ser Ala Met Ser Ser Ser Ala Thr 750
 740 745

Gly Lys Tyr His Phe Ser Asn Leu Val Ser Pro Thr Asn Leu Ser Gln
 755 760 765
 Phe Asn Leu Pro Ala Pro Ser Met Met Arg Ser Ser Ser Ile Pro Ala
 770 775 780
 Gln Asp Ser Ser Phe Asp Leu Tyr Asp Asp Ala Gln Leu Cys Gly Ser
 785 790 795 800
 Ala Thr Ser Leu Glu Glu Arg Pro Arg Ala Val Ser His Ser Gly Ser
 805 810 815
 Phe Arg Asp Ser Met Glu Glu Val His Gly Ser Ser Leu Ser Leu Val
 820 825 830
 Ser Ser Thr Ser Ser Leu Tyr Ser Thr Ala Glu Glu Lys Ala His Ser
 835 840 845
 Glu Gln Ile His Lys Leu Arg Arg Glu Leu Val Ala Ser Gln Glu Lys
 850 855 860
 Val Ala Thr Leu Thr Ser Gln Leu Ser Ala Asn Ala His Leu Val Ala
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 885 890 895
 Thr Met Thr Ala Glu Gln Lys Glu Ser Glu Leu Ile Glu Leu Arg Glu
 900 905 910
 Thr Ile Glu Met Leu Lys Ala Gln Asn Ser Ala Ala Gln Ala Ala Ile
 915 920 925
 Gln Gly Ala Leu Asn Gly Pro Asp His Pro Pro Lys Asp Leu Arg Ile
 930 935 940
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ccaatgcagg aaggaaaacc agcctggacg ggtcccagaa tcaagatgat gttgtcctgc	240
acgtgagctc gaagaccacc ctccagtacc gtagtttgcc ccgcccttct aagtccagca	300
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37

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48

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gtc ctc tct ctc ccc ctc ctc ctc ccc cgc ctc ctc ctc ctg cgc tcc Val Leu Ser Leu Pro Leu Leu Leu Pro Arg Leu Leu Leu Leu Arg Ser	240
cgc ccc ctg ccc cct ccc ccc gtg cct gca gac gcg cgg atc gtc cat Arg Pro Leu Pro Pro Pro Pro Val Pro Ala Asp Ala Arg Ile Val His	288
gcg ctc ctc gcg ggc aga atg ctg ggc agc agc gtc aag agc gtg cag Ala Leu Leu Ala Gly Arg Met Leu Gly Ser Ser Val Lys Ser Val Gln	336
ccc gag gtg gag ctg agc agc ggc ggc ggc gac gag ggc gcg gac gaa Pro Glu Val Glu Leu Ser Ser Gly Gly Gly Asp Glu Gly Ala Asp Glu	384
ccg cgg ggc gcc ggc agg aag gcg gca gcg gcg gac ggc aga ggc atg Pro Arg Gly Ala Gly Arg Lys Ala Ala Ala Ala Asp Gly Arg Gly Met	432
ctg ccc aag cgc gcc aag gcg ccc ggc ggc ggc ggc ggc atg gcc aag Leu Pro Lys Arg Ala Lys Ala Pro Gly Gly Gly Gly Gly Met Ala Lys	480
gcc agc gcg gct gag ctg aag gtc ttc aag tcc ggc agc gtg gac agc Ala Ser Ala Ala Glu Leu Lys Val Phe Lys Ser Gly Ser Val Asp Ser	528
cgt gtc ccc ggc ggg ccg ccc gcc tcc aac ctg cgc aag cag aag tca Arg Val Pro Gly Gly Pro Pro Ala Ser Asn Leu Arg Lys Gln Lys Ser	576
ctc acc aac ctc tct ttt ctc acg gac tcc gag aaa aag ctg cag ctt Leu Thr Asn Leu Ser Phe Leu Thr Asp Ser Glu Lys Lys Leu Gln Leu	624
tat gag ccc gaa tgg agc gac gat atg gcc aag gcg ccc aaa ggc tta Tyr Glu Pro Glu Trp Ser Asp Asp Met Ala Lys Ala Pro Lys Gly Leu	672
ggc aag gtg ggg tcc aag ggc cgt gaa gct ccg ctg atg tcc aag acg Gly Lys Val Gly Ser Lys Gly Arg Glu Ala Pro Leu Met Ser Lys Thr	720

ctg tcc aag tcg gag cac tcg ctc ttc cag gcc aag ggc agc ccg gcg Leu Ser Lys Ser Glu His Ser Leu Phe Gln Ala Lys Gly Ser Pro Ala	768
ggc ggc gcc aag acc ccc ctg gct ccg ctc gcg ccc aac ctg gga aag Gly Gly Ala Lys Thr Pro Leu Ala Pro Leu Ala Pro Asn Leu Gly Lys	816
ccg agc cgg atc cct cga gga ccc tat gcg gag gtc aag ccg ctc agc Pro Ser Arg Ile Pro Arg Gly Pro Tyr Ala Glu Val Lys Pro Leu Ser	864
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ctg ctc tcc agc aag gcc aag gcg caa aag agc tct ggg cct gtc ccc Leu Leu Ser Ser Lys Ala Lys Ala Gln Lys Ser Ser Gly Pro Val Pro	960
tct gcc aag ggc cag gag gag cgc gcc ttc ctc aag gtg gac ccc gag Ser Ala Lys Gly Gln Glu Glu Arg Ala Phe Leu Lys Val Asp Pro Glu	1008
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gat ctc cgg cag aac ctg gaa gag acc atg tcc agc ctg cga ggg tcc Asp Leu Arg Gln Asn Leu Glu Glu Thr Met Ser Ser Leu Arg Gly Ser	1152
cag gtg act cac agc tcc ctg gag atg acc tgc tac gac agc gat gat Gln Val Thr His Ser Ser Leu Glu Met Thr Cys Tyr Asp Ser Asp Asp	1200
gcc aac cca cgc agc gtg tcc agc ctc tcc aac cgc tcg tac cct ctg Ala Asn Pro Arg Ser Val Ser Ser Leu Ser Asn Arg Ser Tyr Pro Leu	1248
tca tgg cgc tat ggc cag tcc agt ccg cgg ctg cag gct ggt gac gcg Ser Trp Arg Tyr Gly Gln Ser Ser Pro Arg Leu Gln Ala Gly Asp Ala	1296
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atg cac ggc gaa cgg gcc cac tac tcc cac acc atg ccc atg cgc agc Met His Gly Glu Arg Ala His Tyr Ser His Thr Met Pro Met Arg Ser	1392

ccc agc aag ctc agc cat atc tcc cgc ctg gag ctg gtc gaa tcc ctg Pro Ser Lys Leu Ser His Ile Ser Arg Leu Glu Leu Val Glu Ser Leu	1440
gac tcg gat gag gtg gac ctc aag tcc ggc tac atg agc gac agt gac Asp Ser Asp Glu Val Asp Leu Lys Ser Gly Tyr Met Ser Asp Ser Asp	1488
ctc atg ggc aag acc atg acg gag gat gat gac atc act acc ggc tgg Leu Met Gly Lys Thr Met Thr Glu Asp Asp Asp Ile Thr Thr Gly Trp	1536
gat gaa agc agc tcc atc agt agt gga ctc agc gat gcc tca gac aat Asp Glu Ser Ser Ser Ile Ser Ser Gly Leu Ser Asp Ala Ser Asp Asn	1584
ctc agt tca gaa gaa ttc aat gcc agc tcc tca ctc aac tcc ctc cca Leu Ser Ser Glu Glu Phe Asn Ala Ser Ser Ser Leu Asn Ser Leu Pro	1632
agt act ccc act gct tct cgc agg aac tca aca ata gtg cta cgc aca Ser Thr Pro Thr Ala Ser Arg Arg Asn Ser Thr Ile Val Leu Arg Thr	1680
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agc tgt gat gat tca tcc aag ggt gga gaa ctg aaa aag ccc atc agc Ser Cys Asp Asp Ser Ser Lys Gly Gly Glu Leu Lys Lys Pro Ile Ser	1872
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 50 55 60

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cac agt tcc tcg gac gtc acc atc ggc ccc cgg ctc ttc ctg tca tgc His Ser Ser Ser Asp Val Thr Ile Gly Pro Arg Leu Phe Leu Ser Cys	6718
ccc atc gat gtg gac ggc tcg aga gtg tgg ttc acc gac ttg tgg aac Pro Ile Asp Val Asp Gly Ser Arg Val Trp Phe Thr Asp Leu Trp Asn	6766
tat tcc att atc ccc tat ctc ctg gaa gcc gtc aga gaa gga ctc cag Tyr Ser Ile Ile Pro Tyr Leu Leu Glu Ala Val Arg Glu Gly Leu Gln	6814
ctc tat gga agg cgc gcc ccc tgg gag gat cct gcc aag tgg gtg atg Leu Tyr Gly Arg Arg Ala Pro Trp Glu Asp Pro Ala Lys Trp Val Met	6862
gac aca tat cca tgg gca gcc agc cca caa cag cac gag tgg cct ccc Asp Thr Tyr Pro Trp Ala Ala Ser Pro Gln Gln His Glu Trp Pro Pro	6910
ctg ctg cag tta cgg cct gag gat gtc ggc ttc gac ggc tac tcc atg Leu Leu Gln Leu Arg Pro Glu Asp Val Gly Phe Asp Gly Tyr Ser Met	6958
cct cgg gag gga tcg aca agc aag cag atg ccc ccc agt gat gct gaa Pro Arg Glu Gly Ser Thr Ser Lys Gln Met Pro Pro Ser Asp Ala Glu	7006
ggc gac ccg ctg atg aac atg ctg atg agg ctg cag gag gca gcc aac Gly Asp Pro Leu Met Asn Met Leu Met Arg Leu Gln Glu Ala Ala Asn	7054
tac tcc agc ccc cag agc tat gac agc gac tcc aac agc aac agc cat Tyr Ser Ser Pro Gln Ser Tyr Asp Ser Asp Ser Asn Ser Asn Ser His	7102
cac gat gac atc ttg gac tcc tct ttg gag tcc act ctg tgacaggggc His Asp Asp Ile Leu Asp Ser Ser Leu Glu Ser Thr Leu	7151
ccggagccca gcgcctctct cttctctctca ccgcattcca cctgcatccc ccacatcacc	7211
ctgaagatga cttcctgagc cagccccag ccacagcctt agagctgcgg gaacaccgag	7271
acccccgctc cttcagcctc gacctgggtg caggcatccc gggccagctg cctgeggacc	7331
gcttccttcc acagcgagaa ctgcactacc ttctgttgta ctttaattat tgttttgct	7391
tggtgctgtg acctccctaa gacactgaag atacttctcg ggaaaggatc atcgccgttg	7451
aaatgaaaag agagacagag agagaaaaaa aaaagagaac ccacatgaag ctctgaaacc	7511

aaacagcatc ctgccatgag cttcccagag acagaagaga ctggagcaaa gtcggaaaca 7571
 cagagaagca cggcttcccc tcagcacaga ccctccagac tgggtctcag agccgtgcca 7631
 cccaccctcc cacacagccg gccacagga gaactggtgc taaccagggt gcttgctttg 7691
 gtcacgttca acgcactaca gagctacgac acaggggaac cttaggagca aataaaccgt 7751
 gctttcatgt tttttaaaaa aaaaaaaaaa aa 7783

<210> 27
 <211> 2380
 <212> PRT
 <213> Homo sapiens

<400> 27

Asn	Gln	Pro	Glu	Arg	Leu	Asn	Ser	Gln	Val	Leu	Gln	Gly	Leu	Gln	Glu	
1					5				10					15		
Pro	Ala	Gly	Glu	Gly	Leu	Pro	Leu	Arg	Lys	Ser	Gly	Ser	Val	Glu	Asn	
		20						25					30			
Gly	Phe	Asp	Thr	Gln	Ile	Tyr	Thr	Asp	Trp	Ala	Asn	His	Tyr	Leu	Ala	
		35					40					45				
Lys	Ser	Gly	His	Lys	Arg	Leu	Ile	Arg	Asp	Leu	Gln	Gln	Asp	Val	Thr	
	50					55					60					
Asp	Gly	Val	Leu	Leu	Ala	Gln	Ile	Ile	Gln	Val	Val	Ala	Asn	Glu	Lys	
65					70				75					80		
Ile	Glu	Asp	Ile	Asn	Gly	Cys	Pro	Lys	Asn	Arg	Ser	Gln	Met	Ile	Glu	
			85						90					95		
Asn	Ile	Asp	Ala	Cys	Leu	Asn	Phe	Leu	Ala	Ala	Lys	Gly	Ile	Asn	Ile	
		100						105					110			
Gln	Gly	Leu	Ser	Ala	Glu	Glu	Ile	Arg	Asn	Gly	Asn	Leu	Lys	Ala	Ile	
		115					120					125				
Leu	Gly	Leu	Phe	Phe	Ser	Leu	Ser	Arg	Tyr	Lys	Gln	Gln	Gln	Gln	Gln	
	130					135					140					
Pro	Gln	Lys	Gln	His	Leu	Ser	Ser	Pro	Leu	Pro	Pro	Ala	Val	Ser	Gln	
145					150					155				160		
Val	Ala	Gly	Ala	Pro	Ser	Gln	Cys	Gln	Ala	Gly	Thr	Pro	Gln	Gln	Gln	
			165						170					175		
Val	Pro	Val	Thr	Pro	Gln	Ala	Pro	Cys	Gln	Pro	His	Gln	Pro	Ala	Pro	
		180						185					190			
His	Gln	Gln	Ser	Lys	Ala	Gln	Ala	Glu	Met	Gln	Ser	Arg	Leu	Pro	Gly	

195	200	205
Pro Thr Ala Arg Val Ser Ala Ala Gly Ser Glu Ala Lys Thr Arg Gly		
210	215	220
Gly Ser Thr Thr Ala Asn Asn Arg Arg Ser Gln Ser Phe Asn Asn Tyr		
225	230	235 240
Asp Lys Ser Lys Pro Val Thr Ser Pro Pro Pro Pro Ser Ser His		
	245	250 255
Glu Lys Glu Pro Leu Ala Ser Ser Ala Ser Ser His Pro Gly Met Ser		
	260	265 270
Asp Asn Ala Pro Ala Ser Leu Glu Ser Gly Ser Ser Ser Thr Pro Thr		
	275	280 285
Asn Cys Ser Thr Ser Ser Ala Ile Pro Gln Pro Gly Ala Ala Thr Lys		
	290	295 300
Pro Trp Arg Ser Lys Ser Leu Ser Val Lys His Ser Ala Thr Val Ser		
305	310	315 320
Met Leu Ser Val Lys Pro Pro Gly Pro Glu Ala Pro Arg Pro Thr Pro		
	325	330 335
Glu Ala Met Lys Pro Ala Pro Asn Asn Gln Lys Ser Met Leu Glu Lys		
	340	345 350
Leu Lys Leu Phe Asn Ser Lys Gly Gly Ser Lys Ala Gly Glu Gly Pro		
	355	360 365
Gly Ser Arg Asp Thr Ser Cys Glu Arg Leu Glu Thr Leu Pro Ser Phe		
	370	375 380
Glu Glu Ser Glu Glu Leu Glu Ala Ala Ser Arg Met Leu Thr Thr Val		
385	390	395 400
Gly Pro Ala Ser Ser Ser Pro Lys Ile Ala Leu Lys Gly Ile Ala Gln		
	405	410 415
Arg Thr Phe Ser Arg Ala Leu Thr Asn Lys Lys Ser Ser Leu Lys Gly		
	420	425 430
Asn Glu Lys Glu Lys Glu Lys Gln Gln Arg Glu Lys Asp Lys Glu Lys		
	435	440 445
Ser Lys Asp Leu Ala Lys Arg Ala Ser Val Thr Glu Arg Leu Asp Leu		
	450	455 460
Lys Glu Glu Pro Lys Glu Asp Pro Ser Gly Ala Ala Val Pro Glu Met		
465	470	475 480
Pro Lys Lys Ser Ser Lys Ile Ala Ser Phe Ile Pro Lys Gly Gly Lys		
	485	490 495

Leu Asn Ser Ala Lys Lys Glu Pro Met Ala Pro Ser His Ser Gly Ile
 500 505 510
 Pro Lys Pro Gly Met Lys Ser Met Pro Gly Lys Ser Pro Ser Ala Pro
 515 520 525
 Ala Pro Ser Lys Glu Gly Glu Arg Ser Arg Ser Gly Lys Leu Ser Ser
 530 535 540
 Gly Leu Pro Gln Gln Lys Pro Gln Leu Asp Gly Arg His Ser Ser Ser
 545 550 555 560
 Ser Ser Ser Leu Ala Ser Ser Glu Gly Lys Gly Pro Gly Gly Thr Thr
 565 570 575
 Leu Asn His Ser Ile Ser Ser Gln Thr Val Ser Gly Ser Val Gly Thr
 580 585 590
 Thr Gln Thr Thr Gly Ser Asn Thr Val Ser Val Gln Leu Pro Gln Pro
 595 600 605
 Gln Gln Gln Tyr Asn His Pro Asn Thr Ala Thr Val Ala Pro Phe Leu
 610 615 620
 Tyr Arg Ser Gln Thr Asp Thr Glu Gly Asn Val Thr Ala Glu Ser Ser
 625 630 635 640
 Ser Thr Gly Val Ser Val Glu Pro Ser His Phe Thr Lys Thr Gly Gln
 645 650 655
 Pro Ala Leu Glu Glu Leu Thr Gly Glu Asp Pro Glu Ala Arg Arg Leu
 660 665 670
 Arg Thr Val Lys Asn Ile Ala Asp Leu Arg Gln Asn Leu Glu Glu Thr
 675 680 685
 Met Ser Ser Leu Arg Gly Thr Gln Val Thr His Ser Thr Leu Glu Thr
 690 695 700
 Thr Phe Asp Thr Asn Val Thr Thr Glu Met Ser Gly Arg Ser Ile Leu
 705 710 715 720
 Ser Leu Thr Gly Arg Pro Thr Pro Leu Ser Trp Arg Leu Gly Gln Ser
 725 730 735
 Ser Pro Arg Leu Gln Ala Gly Asp Ala Pro Ser Met Gly Asn Gly Tyr
 740 745 750
 Pro Pro Arg Ala Asn Ala Ser Arg Phe Ile Asn Thr Glu Ser Gly Arg
 755 760 765
 Tyr Val Tyr Ser Ala Pro Leu Arg Arg Gln Leu Ala Ser Arg Gly Ser
 770 775 780
 Ser Val Cys His Val Asp Val Ser Asp Lys Ala Gly Asp Glu Met Asp
 785 790 795 800

Leu Glu Gly Ile Ser Met Asp Ala Pro Gly Tyr Met Ser Asp Gly Asp
 805 810 815
 Val Leu Ser Lys Asn Ile Arg Thr Asp Asp Ile Thr Ser Gly Tyr Met
 820 825 830
 Thr Asp Gly Gly Leu Gly Leu Tyr Thr Arg Arg Leu Asn Arg Leu Pro
 835 840 845
 Asp Gly Met Ala Val Val Arg Glu Thr Leu Gln Arg Asn Thr Ser Leu
 850 855 860
 Gly Leu Gly Asp Ala Asp Ser Trp Asp Asp Ser Ser Ser Val Ser Ser
 865 870 875 880
 Gly Ile Ser Asp Thr Ile Asp Asn Leu Ser Thr Asp Asp Ile Asn Thr
 885 890 895
 Ser Ser Ser Ile Ser Ser Tyr Ala Asn Thr Pro Ala Ser Ser Arg Lys
 900 905 910
 Asn Leu Asp Val Gln Thr Asp Ala Glu Lys His Ser Gln Val Glu Arg
 915 920 925
 Asn Ser Leu Trp Ser Gly Asp Asp Val Lys Lys Ser Asp Gly Gly Ser
 930 935 940
 Asp Ser Gly Ile Lys Met Glu Pro Gly Ser Lys Trp Arg Arg Asn Pro
 945 950 955 960
 Ser Asp Val Ser Asp Glu Ser Asp Lys Ser Thr Ser Gly Lys Lys Asn
 965 970 975
 Pro Val Ile Ser Gln Thr Gly Ser Trp Arg Arg Gly Met Thr Ala Gln
 980 985 990
 Val Gly Ile Thr Met Pro Arg Thr Lys Ala Ser Ala Pro Ala Gly Ala
 995 1000 1005
 Leu Lys Thr Pro Gly Thr Gly Lys Thr Asp Asp Ala Lys Val Ser Glu
 1010 1015 1020
 Lys Gly Arg Leu Ser Pro Lys Ala Ser Gln Val Lys Arg Ser Pro Ser
 1025 1030 1035 1040
 Asp Ala Gly Arg Ser Ser Gly Asp Glu Ser Lys Lys Pro Leu Pro Ser
 1045 1050 1055
 Ser Ser Arg Thr Pro Thr Ala Asn Ala Asn Ser Phe Gly Phe Lys Lys
 1060 1065 1070
 Gln Ser Gly Ser Ala Thr Gly Leu Ala Met Ile Thr Ala Ser Gly Val
 1075 1080 1085
 Thr Val Thr Ser Arg Ser Ala Thr Leu Gly Lys Ile Pro Lys Ser Ser

1395

1400

1405

Ser Pro Ala Ala Ser Pro Lys Phe Cys Arg Ser Thr Leu Pro Arg Lys
 1410 1415 1420
 Gln Asp Ser Asp Pro His Leu Asp Arg Asn Thr Leu Pro Lys Lys Gly
 1425 1430 1435 1440
 Leu Arg Tyr Thr Pro Thr Ser Gln Leu Arg Thr Gln Glu Asp Ala Lys
 1445 1450 1455
 Glu Trp Leu Arg Ser His Ser Ala Gly Gly Leu Gln Asp Thr Ala Ala
 1460 1465 1470
 Asn Ser Pro Phe Ser Ser Gly Ser Ser Val Thr Ser Pro Ser Gly Thr
 1475 1480 1485
 Arg Phe Asn Phe Ser Gln Leu Ala Ser Pro Thr Thr Val Thr Gln Met
 1490 1495 1500
 Ser Leu Ser Asn Pro Thr Met Leu Arg Thr His Ser Leu Ser Asn Ala
 1505 1510 1515 1520
 Asp Gly Gln Tyr Asp Pro Tyr Thr Asp Ser Arg Phe Arg Asn Ser Ser
 1525 1530 1535
 Met Ser Leu Asp Glu Lys Ser Arg Thr Met Ser Arg Ser Gly Ser Phe
 1540 1545 1550
 Arg Asp Gly Phe Glu Glu Val His Gly Ser Ser Leu Ser Leu Val Ser
 1555 1560 1565
 Ser Thr Ser Ser Val Tyr Ser Thr Pro Glu Glu Lys Cys Gln Ser Glu
 1570 1575 1580
 Ile Arg Lys Leu Arg Arg Glu Leu Asp Ala Ser Gln Glu Lys Val Ser
 1585 1590 1595 1600
 Ala Leu Thr Thr Gln Leu Thr Ala Asn Ala His Leu Val Ala Ala Phe
 1605 1610 1615
 Glu Gln Ser Leu Gly Asn Met Thr Ile Arg Leu Gln Ser Leu Thr Met
 1620 1625 1630
 Thr Ala Glu Gln Lys Asp Ser Glu Leu Asn Glu Leu Arg Lys Thr Ile
 1635 1640 1645
 Glu Leu Leu Lys Lys Gln Asn Ala Ala Ala Gln Ala Ala Ile Asn Gly
 1650 1655 1660
 Val Ile Asn Thr Pro Glu Leu Asn Cys Lys Gly Asn Gly Thr Ala Gln
 1665 1670 1675 1680
 Ser Ala Asp Leu Arg Ile Arg Arg Gln His Ser Ser Asp Ser Val Ser
 1685 1690 1695

Ser Ile Asn Ser Ala Thr Ser His Ser Ser Val Gly Ser Asn Ile Glu
 1700 1705 1710

Ser Asp Ser Lys Lys Lys Lys Arg Lys Asn Trp Val Asn Glu Leu Arg
 1715 1720 1725

Ser Ser Phe Lys Gln Ala Phe Gly Lys Lys Lys Ser Pro Lys Ser Ala
 1730 1735 1740

Ser Ser His Ser Asp Ile Glu Glu Met Thr Asp Ser Ser Leu Pro Ser
 1745 1750 1755 1760

Ser Pro Lys Leu Pro His Asn Gly Ser Thr Gly Ser Thr Pro Leu Leu
 1765 1770 1775

Arg Asn Ser His Ser Asn Ser Leu Ile Ser Glu Cys Met Asp Ser Glu
 1780 1785 1790

Ala Glu Thr Val Met Gln Leu Arg Asn Glu Leu Arg Asp Lys Glu Met
 1795 1800 1805

Lys Leu Thr Asp Ile Arg Leu Glu Ala Leu Ser Ser Ala His Gln Leu
 1810 1815 1820

Asp Gln Leu Arg Glu Ala Met Asn Arg Met Gln Ser Glu Ile Glu Lys
 1825 1830 1835 1840

Leu Lys Ala Glu Asn Asp Arg Leu Lys Ser Glu Ser Gln Gly Ser Gly
 1845 1850 1855

Cys Ser Arg Ala Pro Ser Gln Val Ser Ile Ser Ala Ser Pro Arg Gln
 1860 1865 1870

Ser Met Gly Leu Ser Gln His Ser Leu Asn Leu Thr Glu Ser Thr Ser
 1875 1880 1885

Leu Asp Met Leu Leu Asp Asp Thr Gly Glu Cys Ser Ala Arg Lys Glu
 1890 1895 1900

Gly Gly Arg His Val Lys Ile Val Val Ser Phe Gln Glu Glu Met Lys
 1905 1910 1915 1920

Trp Lys Glu Asp Ser Arg Pro His Leu Phe Leu Ile Gly Cys Ile Gly
 1925 1930 1935

Val Ser Gly Lys Thr Lys Trp Asp Val Leu Asp Gly Val Val Arg Arg
 1940 1945 1950

Leu Phe Lys Glu Tyr Ile Ile His Val Asp Pro Val Ser Gln Leu Gly
 1955 1960 1965

Leu Asn Ser Asp Ser Val Leu Gly Tyr Ser Ile Gly Glu Ile Lys Arg
 1970 1975 1980

Ser Asn Thr Ser Glu Thr Pro Glu Leu Leu Pro Cys Gly Tyr Leu Val
 1985 1990 1995 2000

Gly Glu Asn Thr Thr Ile Ser Val Thr Val Lys Gly Leu Ala Glu Asn
 2005 2010 2015
 Ser Leu Asp Ser Leu Val Phe Glu Ser Leu Ile Pro Lys Pro Ile Leu
 2020 2025 2030
 Gln Arg Tyr Val Ser Leu Leu Ile Glu His Arg Arg Ile Ile Leu Ser
 2035 2040 2045
 Gly Pro Ser Gly Thr Gly Lys Thr Tyr Leu Ala Asn Arg Leu Ser Glu
 2050 2055 2060
 Tyr Ile Val Leu Arg Glu Gly Arg Glu Leu Thr Asp Gly Val Ile Ala
 2065 2070 2075 2080
 Thr Phe Asn Val Asp His Lys Ser Ser Lys Glu Leu Arg Gln Tyr Leu
 2085 2090 2095
 Ser Asn Leu Ala Asp Gln Cys Asn Ser Glu Asn Asn Ala Val Asp Met
 2100 2105 2110
 Pro Leu Val Ile Ile Leu Asp Asn Leu His His Val Ser Ser Leu Gly
 2115 2120 2125
 Glu Ile Phe Asn Gly Leu Leu Asn Cys Lys Tyr His Lys Cys Pro Tyr
 2130 2135 2140
 Ile Ile Gly Thr Met Asn Gln Ala Thr Ser Ser Thr Pro Asn Leu Gln
 2145 2150 2155 2160
 Leu His His Asn Phe Arg Trp Val Leu Cys Ala Asn His Thr Glu Pro
 2165 2170 2175
 Val Lys Gly Phe Leu Gly Arg Phe Leu Arg Arg Lys Leu Met Glu Thr
 2180 2185 2190
 Glu Ile Ser Gly Arg Val Arg Asn Met Glu Leu Val Lys Ile Ile Asp
 2195 2200 2205
 Trp Ile Pro Lys Val Trp His His Leu Asn Arg Phe Leu Glu Ala His
 2210 2215 2220
 Ser Ser Ser Asp Val Thr Ile Gly Pro Arg Leu Phe Leu Ser Cys Pro
 2225 2230 2235 2240
 Ile Asp Val Asp Gly Ser Arg Val Trp Phe Thr Asp Leu Trp Asn Tyr
 2245 2250 2255
 Ser Ile Ile Pro Tyr Leu Leu Glu Ala Val Arg Glu Gly Leu Gln Leu
 2260 2265 2270
 Tyr Gly Arg Arg Ala Pro Trp Glu Asp Pro Ala Lys Trp Val Met Asp
 2275 2280 2285
 Thr Tyr Pro Trp Ala Ala Ser Pro Gln Gln His Glu Trp Pro Pro Leu

2290

2295

2300

Leu Gln Leu Arg Pro Glu Asp Val Gly Phe Asp Gly Tyr Ser Met Pro
 2305 2310 2315 2320

Arg Glu Gly Ser Thr Ser Lys Gln Met Pro Pro Ser Asp Ala Glu Gly
 2325 2330 2335

Asp Pro Leu Met Asn Met Leu Met Arg Leu Gln Glu Ala Ala Asn Tyr
 2340 2345 2350

Ser Ser Pro Gln Ser Tyr Asp Ser Asp Ser Asn Ser Asn Ser His His
 2355 2360 2365

Asp Asp Ile Leu Asp Ser Ser Leu Glu Ser Thr Leu
 2370 2375 2380

<210> 28
 <211> 96
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(93)

<400> 28

agc agg gag agg gga ggg agt gtg ccg tct ctt ctg caa ggg cag tgc 48
 Ser Arg Glu Arg Gly Gly Ser Val Pro Ser Leu Leu Gln Gly Gln Cys

ccc agc ctc agc cac act tct gat ctg cag tcc aac aga cct ttc tag 96
 Pro Ser Leu Ser His Thr Ser Asp Leu Gln Ser Asn Arg Pro Phe *

<210> 29
 <211> 75
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(72)

<400> 29

cat gcc aaa gag aac ctg ggg gtg cca ggg ggt cct cag agc tca cac 48
 His Ala Lys Glu Asn Leu Gly Val Pro Gly Gly Pro Gln Ser Ser His

tgc act tgt ggc acc cac agc gag tag 75
 Cys Thr Cys Gly Thr His Ser Glu *

<210> 30
 <211> 489
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(489)

<400> 30

cca tcc gtg agc cga gga aac tgt aca cag atc tac aca gac tgg gcc Pro Ser Val Ser Arg Gly Asn Cys Thr Gln Ile Tyr Thr Asp Trp Ala	48
aat cat tac cta gcc aaa tcc ggc cac aag cgt ctc atc aag gat ctc Asn His Tyr Leu Ala Lys Ser Gly His Lys Arg Leu Ile Lys Asp Leu	96
cag caa gat gtg aca gat ggc gtc ctc ctg gcc cag att atc cag gtt Gln Gln Asp Val Thr Asp Gly Val Leu Leu Ala Gln Ile Ile Gln Val	144
gtg gca aat gaa aag att gaa gac atc aat ggc tgt ccg aag aac aga Val Ala Asn Glu Lys Ile Glu Asp Ile Asn Gly Cys Pro Lys Asn Arg	192
tcc caa atg att gaa aac ata gat gcc tgc ttg aat ttc ctg gca gct Ser Gln Met Ile Glu Asn Ile Asp Ala Cys Leu Asn Phe Leu Ala Ala	240
aag gga ata aac atc cag ggg ctg tct gca gaa gag atc agg aat gga Lys Gly Ile Asn Ile Gln Gly Leu Ser Ala Glu Glu Ile Arg Asn Gly	288
aac ctc aag gcc att cta ggc ctc ttc ttc agc ctc tcc cga tac aag Asn Leu Lys Ala Ile Leu Gly Leu Phe Phe Ser Leu Ser Arg Tyr Lys	336
cag cag cag cag cag ccc cag aag cag cac ctc tcc tca cct ctg ccg Gln Gln Gln Gln Gln Pro Gln Lys Gln His Leu Ser Ser Pro Leu Pro	384
ccc gcc gta tcc cag gtg gcc ggg gcc ccc tcc cag tgc cag gct ggc Pro Ala Val Ser Gln Val Ala Gly Ala Pro Ser Gln Cys Gln Ala Gly	432
acc cct cag cag cag gtg cca gtc act ccc caa gcc ccg tgc cag cct Thr Pro Gln Gln Gln Val Pro Val Thr Pro Gln Ala Pro Cys Gln Pro	480
cac cag cca His Gln Pro	489

<210> 31
<211> 31
<212> PRT
<213> Homo sapiens

<400> 31

Ser Arg Glu Arg Gly Gly Ser Val Pro Ser Leu Leu Gln Gly Gln Cys
1 5 10 15

Pro Ser Leu Ser His Thr Ser Asp Leu Gln Ser Asn Arg Pro Phe
20 25 30

<210> 32
<211> 24
<212> PRT
<213> Homo sapiens

<400> 32

His Ala Lys Glu Asn Leu Gly Val Pro Gly Gly Pro Gln Ser Ser His
5 10 15

Cys Thr Cys Gly Thr His Ser Glu
20

<210> 33
<211> 163
<212> PRT
<213> Homo sapiens

<400> 33

Pro Ser Val Ser Arg Gly Asn Cys Thr Gln Ile Tyr Thr Asp Trp Ala
5 10 15

Asn His Tyr Leu Ala Lys Ser Gly His Lys Arg Leu Ile Lys Asp Leu
20 25 30

Gln Gln Asp Val Thr Asp Gly Val Leu Leu Ala Gln Ile Ile Gln Val
35 40 45

Val Ala Asn Glu Lys Ile Glu Asp Ile Asn Gly Cys Pro Lys Asn Arg
50 55 60

Ser Gln Met Ile Glu Asn Ile Asp Ala Cys Leu Asn Phe Leu Ala Ala

Gln Lys Asp Ser Glu Leu Asn Glu Leu Arg Lys Thr Ile Glu Leu Leu

aag aaa cag aat gca gct gcc cag gct gcc att aat gga gtg att aac 383
Lys Lys Gln Asn Ala Ala Ala Gln Ala Ala Ile Asn Gly Val Ile Asn

acg cca gag ctc aac tgc aaa gga aat ggc agt gcc agg cta cag acc 431
Thr Pro Glu Leu Asn Cys Lys Gly Asn Gly Ser Ala Arg Leu Gln Thr

tac gca tcc gca gca aca ctc ctc cga cag tgt ctc cag tat caa tag 479
Tyr Ala Ser Ala Ala Thr Leu Leu Arg Gln Cys Leu Gln Tyr Gln *

<210> 35
<211> 22
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (1)...(21)

<400> 35

cgc cac cag cca ctc aag tgt g 22
Arg His Gln Pro Leu Lys Cys

<210> 36
<211> 158
<212> PRT
<213> mouse

<400> 36

Glu Lys Ser Arg Thr Met Ser Arg Ser Gly Ser Phe Arg Asp Gly Phe
1 5 10 15

Glu Glu Val His Gly Ser Ser Leu Ser Leu Val Ser Ser Thr Ser Ser
20 25 30

Ile Tyr Ser Thr Pro Glu Glu Lys Cys Gln Ser Glu Ile Arg Lys Leu
35 40 45

Arg Arg Glu Leu Asp Ala Ser Gln Glu Lys Val Ser Ala Leu Thr Thr
50 55 60

Gln Leu Thr Ala Asn Ala His Leu Val Ala Ala Phe Glu Gln Ser Leu
65 70 75 80

Gly Asn Met Thr Ile Arg Leu Gln Ser Leu Thr Met Thr Ala Glu Gln
85 90 95

Lys Asp Ser Glu Leu Asn Glu Leu Arg Lys Thr Ile Glu Leu Leu Lys
100 105 110

Lys Gln Asn Ala Ala Ala Gln Ala Ala Ile Asn Gly Val Ile Asn Thr
115 120 125

Pro Glu Leu Asn Cys Lys Gly Asn Gly Ser Ala Arg Leu Gln Thr Tyr
130 135 140

Ala Ser Ala Ala Thr Leu Leu Arg Gln Cys Leu Gln Tyr Gln
145 150 155

<210> 37
<211> 7
<212> PRT
<213> mouse

<400> 37

Arg His Gln Pro Leu Lys Cys
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<210> 38
<211> 19
<212> PRT
<213> artificial Sequence

<220>

<223> Description of the artificial Sequence: Peptide for production of AK

<400> 38

Glu Lys Gly Glu Asp Pro Glu Thr Arg Arg Met Arg Thr Val Lys Asn
5 10 15

Ile Ala Asp

<210> 39
<211> 81369
<212> DNA
<213> Homo sapiens

<400> 39

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tgagggtgca ttgcaaatcc aggctagagg gagagatacc agttaggana gtacagcaat 120

actctactgg gaaatggtga ggtgtttcgt gaagacaatg gcaacacaga tgaagacatg	180
cagatggagg aaataaagat ccagttgagc ttgttggcca gttggataga gggtgaggtt	240
atgcatgatg gagcaatcta ggtttttgtc ttgggtaggt gtttccatga tagtactcag	300
aatgaatcat atagttgtac aggttgaatc ccacccatgt ttgcacaata gagtgactgt	360
ctagctgaaa tccagatgac actctgtatg ctaagctatg cttcatggaa ctgtataaag	420
gcacttgcta cataggctag tggcagatct ggaagtaacc tatatggtat ataggaaatg	480
aggtggcttt tgtataaatc ctacagataa atttcatttc ctgatcctat tattttgact	540
catgttagcc caagaagagt attcagtact tcatatccct gaaggtaaga cagagtagta	600
ttagattcac tatttgcaa ataaaaggga tcaagtccta agatcaagct gatgaatcaa	660
cacctcatag gatattgtccc aaccaattat atggcttccc ctataaataa aatctagttc	720
tcttctctgg agaggaacag tgaagaatat cataacctat gctacaaact gcttgagtag	780
gagctacttc tctccaaggc tttatatcat tcattctggc aggccctct gtttgttctc	840
accagctcct gggaaattta tttctcctct agtgatataa aagctctctg tttgagatga	900
agggctgccc agtttatcag atctgtatta gtctgttctc aggctgctaa taaagacata	960
cctgagactg agtaatttat gaaggaaaga ggtttaattg actcacagtt ccacatggct	1020
ggggaggcct cacaatcatg gcgaaagact aataaggagc aaagtcacat cttacatggc	1080
tgcagacaag agagcatgtg caggggaact gctctccata aaaccatcag atcttgtgag	1140
acttgttcac tattacaaga acaacagaca ggaaaacccg cccctcaat tcaattacct	1200
gccactggga cctcccaca acacatggg attatgagag ctacaattca agatgagatt	1260
tgggtgggga taccgcaaaa ccatatgaag ttctttcttt gttactgggt accatatcca	1320
ttctgttgag gttctgagcc tttccagtta ctgtaactcc tctatctcct gtctgtgcta	1380
agactcagtg acctctctct gccttgettc tgctttgtcc tgacccttc tgtgcatgca	1440
ctcactctag tttgccacc tgaggtgaga gatggtccag attagcaaca acaatctgtg	1500
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